

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Kaufman, Randal J.  
Wasley, Louise

(ii) TITLE OF INVENTION: Method of Increasing Yield of  
Mature Proteins

(iii) NUMBER OF SEQUENCES: 2

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: Massachusetts  
(E) COUNTRY: United States of America  
(F) ZIP: 02140

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: WordPerfect 5.1

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA: not applicable

(A) APPLICATION NUMBER:  
(B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ellen J. Kapinos, Esquire  
(B) REGISTRATION NUMBER: 32,245  
(C) REFERENCE/DOCKET NUMBER: GI 5181

## Patent Application US/07/621,092B

54 (ix) TELECOMMUNICATION INFORMATION:  
55  
56 (A) TELEPHONE: (617) 876-1170  
57 (B) TELEFAX: (617) 876-5851  
58  
59 (2) INFORMATION FOR SEQ ID NO:1  
60  
61 (i) SEQUENCE CHARACTERISTICS:  
62  
63 (A) LENGTH: 2385 base pairs  
64  
65 (B) TYPE: nucleic acid  
66  
67 (C) STRANDEDNESS: double  
68  
69 (D) TOPOLOGY: unknown  
70  
71 (ii) MOLECULE TYPE: partial human genomic DNA  
72  
73 (A) DESCRIPTION: sequence encoding furin  
74  
75 (iii) HYPOTHETICAL: no  
76  
77 (iv) ANTI-SENSE: no  
78  
79 (v) PUBLICATION INFORMATION:  
80  
81 (A) AUTHORS: van den Ouweland, A. M. W.  
82 (B) JOURNAL: Nucl. Acids. Res.  
83 (C) VOLUME: 18  
84 (D) PAGES: 664  
85 (E) DATE: 1990  
86  
87 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:1  
88  
89 ATG GAG CTC AGG CCC TGG TTC 21  
90 Met Glu Leu Arg Pro Trp Leu  
91 1 5  
92  
93 CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA 60  
94 Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu  
95 10 15 20  
96  
97 GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG 99  
98 Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr  
99 25 30  
100  
101 TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC 138  
102 Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn  
103 35 40 45  
104  
105  
106 AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG 177

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107	Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln	
108	50 55	
109		
110	ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG	216
111	Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val	
112	60 65 70	
113		
114		
115	ACG AAG CGG TCC CTG TCG CCT CAC CGC CCG CGG CAC AGC	255
116	Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser	
117	75 80 85	
118		
119		
120	CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG GAA CAG	294
121	Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln	
122	90 95	
123		
124	CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG	333
125	Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln	
126	100 105 110	
127		
128	GAG CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG	372
129	Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu	
130	115 120	
131		
132	TCT GGT GTC ACT CAG CGG GAC CTG AAT GTG AAG GCG GCC	411
133	Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala	
134	125 130 135	
135		
136	TGG GCG CAG GGC TAC ACA GGG CAC GGC ATT CTG GTC TCC	450
137	Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser	
138	140 145 150	
139		
140	ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC CCC GAC TTG	489
141	Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu	
142	155 160	
143		
144	GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT	528
145	Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn	
146	165 170 175	
147		
148	GAC CAG GAC CCT GAC CCC CAG CCT CGG TAC ACA CAG ATG	567
149	Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met	
150	180 185	
151		
152	AAT GAC AAC AGG CAC GGC ACA CGG TGT GCG GGG GAA GTG	606
153	Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val	
154	190 195 200	
155		
156	GCT GCC GTG GCC AAC AAC CGT GTC TGT GGT GTA GGT GTG	645
157	Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val	
158	205 210 215	
159		

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160	GCC TAC AAC GCC CGC ATT GGA GGG GTC CGC ATG CTG GAT	684
161	Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp	
162	220 225	
163		
164	GGC GAG GTG ACA GAT GCA GTG GAG GCA CGC TCG CTG GGC	723
165	Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly	
166	230 235 240	
167		
168	CTG AAC CCC AAC CAC ATC CAC ATC TAC AGT GCC AGC TGG	762
169	Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp	
170	245 250	
171		
172	GGC CCC GAG GAT GAC GGC AAG ACA GTG GAT GGG CCA GCC	801
173	Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala	
174	255 260 265	
175		
176	CGG CTC GCC GAG GAG GCC TTC TTC CGT GGG CTT AGC CAG	840
177	Arg Leu Ala Glu Glu Ala Phe Arg Gly Val Ser Gln	
178	270 275 280	
179		
180	GGC CGA GGG GGG CTG GGC TCC ATC TTT GTC TGG GCC TCG	879
181	Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser	
182	285 290	
183		
184	GGG AAC GGG GGG CGG GAA CAT GAC AGC TGC AAC TGC GAC	918
185	Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp	
186	295 300 305	
187		
188	GGC TAC ACC AAC AGT ATC TAC ACG CTG TCC ATC AGC AGC	957
189	Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser	
190	310 315	
191		
192	GCC ACG CAG TTT GGC AAC GTG CCG TGG TAC AGC GAG GCC	996
193	Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala	
194	320 325 330	
195		
196	TGC TCG TCC ACA CTG GCC ACG ACC TAC AGC AGT GGC AAC	1035
197	Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn	
198	335 340 345	
199		
200	CAG AAT GAG AAG CAG ATC GTG ACG ACT GAC TTG CGG CAG	1074
201	Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln	
202	350 355	
203		
204	AAG TGC ACG GAG TCT CAC ACG GGC ACC TCA GCC TCT GCC	1113
205	Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala	
206	360 365 370	
207		
208	CCC TTA GCA GCC GGC ATC ATT GCT CTC ACC CTG GAG GCC	1152
209	Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala	
210	375 380	
211		
212	AAT AAG AAC CTC ACA TGG CGG GAC ATG CAA CAC CTG GTG	1191

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213	Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val	
214	385					390					395			
215														
216	GTA	CAG	ACC	TCG	AAG	CCA	GCC	CAC	CTC	AAT	GCC	AAC	GAC	1230
217	Val	Gln	Thr	Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp	
218			400					405					410	
219														
220	TGG	GCC	ACC	AAT	GGT	GTG	GGG	CGG	AAA	GTG	AGC	CAC	TCA	1269
221	Trp	Ala	Thr	Asn	Gly	Val	Gly	Arg	Lys	Val	Ser	His	Ser	
222					415					420				
223														
224	TAT	GGC	TAC	GGG	CTT	TTC	GAC	GCA	GGC	GCC	ATG	GTG	GCC	1308
225	Tyr	Gly	Tyr	Gly	Leu	Leu	Asp	Ala	Gly	Ala	Met	Val	Ala	
226		425					430					435		
227														
228	CTG	GCC	CAG	AAT	TGG	ACC	ACA	GTC	GCC	CCC	CAG	CGG	AAG	1347
229	Leu	Ala	Gln	Asn	Trp	Thr	Thr	Val	Ala	Pro	Gln	Arg	Lys	
230				440						445				
231														
232	TGC	ATC	ATC	GAC	ATC	CTC	ACC	GAG	CCC	AAA	GAC	ATC	GGG	1386
233	Cys	Ile	Ile	Asp	Ile	Leu	Thr	Glu	Pro	Lys	Asp	Ile	Gly	
234	450					455					460			
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236	AAA	CGG	CTC	GAC	CTC	CGG	AAC	ACC	GTG	ACC	GCG	TCC	CTG	1425
237	Lys	Arg	Leu	Glu	Val	Arg	Lys	Thr	Val	Thr	Ala	Cys	Leu	
238			465					470					475	
239														
240	GGC	GAG	CCC	AAC	CAC	ATC	ACT	CGG	CTG	GAG	CAC	GCT	CAG	1464
241	Gly	Glu	Pro	Asn	His	Ile	Thr	Arg	Leu	Glu	His	Ala	Gln	
242					480					485				
243														
244	GCG	CGG	CTC	ACC	CTG	TCC	TAT	AAT	CGC	CGT	GGC	GAC	CTG	1503
245	Ala	Arg	Leu	Thr	Leu	Ser	Tyr	Asn	Arg	Arg	Gly	Asp	Leu	
246		490					495					500		
247														
248	GCC	ATC	CAC	CTG	GTC	AGC	CCC	ATG	GGC	ACC	CGC	TCC	ACC	1542
249	Ala	Ile	His	Leu	Val	Ser	Pro	Met	Gly	Thr	Arg	Ser	Thr	
250				505					510					
251														
252	CTG	CTG	GCA	GCC	AGG	CCA	CAT	GAC	TAC	TCC	GCA	GAT	GGG	1581
253	Leu	Leu	Ala	Ala	Arg	Pro	His	Asp	Tyr	Ser	Ala	Asp	Gly	
254	515					520					525			
255														
256	TTT	AAT	GAC	TGG	GCC	TTC	ATG	ACA	ACT	CAT	TCC	TGG	GAT	1620
257	Phe	Asn	Asp	Trp	Ala	Phe	Met	Thr	Thr	His	Ser	Trp	Asp	
258			530					535					540	
259														
260	GAC	GAT	CCC	TCT	GGG	GAG	TGG	GTC	CTA	GAG	ATT	GAA	AAC	1659
261	Glu	Asp	Pro	Ser	Gly	Glu	Trp	Val	Leu	Glu	Ile	Glu	Asn	
262					545					550				
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264	ACC	AGC	GAA	GCC	AAC	AAC	TAT	GGG	ACG	CTG	ACC	AAC	TCC	1698
265	Thr	Ser	Glu	Ala	Asn	Asn	Tyr	Gly	Thr	Leu	Thr	Lys	Phe	

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266	555	560	565	
267				
268	ACC CTC GTA CTC TAT GGC ACC GCC CCT GAC GGG CTC CCC	1737		
269	Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro			
270	570 575			
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272	GTA CCT CCA GAA AGC AGT GGC TGC AAG ACC CTC ACG TCC	1776		
273	Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser			
274	580 585 590			
275				
276	AGT CAG GCC TGT GTG GTG TGC GAG GAA GGC TTC TCC CTC	1815		
277	Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu			
278	595 600 605			
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280	CAC CAG AAG AGC TGT GTC CAG CAC TGC CCT CCA GGC TTC	1854		
281	His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe			
282	610 615			
283				
284	GCC CCC CAA GTC CTC GAT ACG CAC TAT AGC ACC GAG AAT	1893		
285	Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn			
286	620 625 630			
287				
288	GAC GTG GAG ACC ATC CGG GCC AGC GTC TGC GCC CCC TGC	1932		
289	Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys			
290	635 640			
291				
292	CAC GCC TCA TGT GCC ACA TGC CAG GGG CCG GCC CTG ACA	1971		
293	His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr			
294	645 650 655			
295				
296	GAC TGC CTC AGC TGC CCC AGC CAC GCC TCC TTG GAC CCT	2010		
297	Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro			
298	660 665 670			
299				
300	GTG GAG CAG ACT TGC TCC CGG CAA AGC CAG AGC AGC CGA	2049		
301	Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg			
302	675 680			
303				
304	GAG TCC CCG CCA CAG CAG CAG CCA CCT CGG CTG CCC CCG	2088		
305	Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro			
306	685 690 695			
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308	GAG GTG GAG GCG GGG CAA CGG CTG CGG GCA GGG CTG CTG	2127		
309	Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu			
310	700 705			
311				
312	CCC TCA CAC CTG CCT GAG GTG GTG GCC GGC CTC AGC TGC	2166		
313	Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys			
314	710 715 720			
315				
316	GCC TTC ATC GTG CTG GTC TTC GTC ACT GTC TTC CTG CTC	2205		
317	Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val			
318	725 730 735			

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319  
320 CTG CAG CTG CGC TCT GGC TTT AGT TTT CGG GGG GTG AAG 2244  
321 Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys  
322 740 745  
323  
324 GTG TAC ACC ATG GAC CGT GGC CTC ATC TCC TAC AAG GGG 2283  
325 Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly  
326 750 755 760  
327  
328 CTG CCC CCT GAA GCC TGG CAG GAG GAG TGC CCG TCT GAC 2322  
329 Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp  
330 765 770  
331  
332 TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT 2361  
333 Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe  
334 775 780 785  
335  
336 ATC AAA GAC CAG AGC GCC CTC TGA 2385  
337 Ile Lys Asp Gln Ser Ala Leu End  
338 790  
339  
340

## 341 (3) INFORMATION FOR SEQ ID NO:2

342

## 343 (i) SEQUENCE CHARACTERISTICS:

344

345 (A) LENGTH: 794 amino acids

346

347 (B) TYPE: amino acids

348

349 (C) STRANDEDNESS: single

350

351 (D) TOPOLOGY: unknown

352

353 (ii) MOLECULE TYPE: furin

354

355 (iii) HYPOTHETICAL: no

356

357 (iv) ANTI-SENSE: no

358

## 359 (v) PUBLICATION INFORMATION:

360

361 (A) AUTHORS: van den Ouweland, A. M. W.

362 (B) JOURNAL: Nucl. Acids. Res.

363 (C) VOLUME: 18

364 (D) PAGES: 664

365 (E) DATE: 1990

366

## 367 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

368

369

370 Met Glu Leu Arg Pro Trp Leu

371 1

5

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372  
373 Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu  
374 10 15 20  
375  
376 Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr  
377 25 30  
378  
379 Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn  
380 35 40 45  
381  
382 Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln  
383 50 55  
384  
385 Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val  
386 60 65 70  
387  
388 Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser  
389 75 80 85  
390  
391  
392 Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln  
393 90 95  
394  
395 Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln  
396 100 105 110  
397  
398 Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu  
399 115 120  
400  
401 Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala  
402 125 130 135  
403  
404 Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser  
405 140 145 150  
406  
407 Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu  
408 155 160  
409  
410 Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn  
411 165 170 175  
412  
413 Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met  
414 180 185  
415  
416 Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val  
417 190 195 200  
418  
419 Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val  
420 205 210 215  
421  
422 Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp  
423 220 225  
424



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425 Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly  
426 230 235 240  
427  
428 Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp  
429 245 250  
430  
431 Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala  
432 255 260 265  
433  
434 Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln  
435 270 275 280  
436  
437 Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser  
438 285 290  
439  
440 Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp  
441 295 300 305  
442  
443 Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser  
444 310 315  
445  
446  
447 Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala  
448 320 325 330  
449  
450 Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn  
451 335 340 345  
452  
453 Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln  
454 350 355  
455  
456 Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala  
457 360 365 370  
458  
459 Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala  
460 375 380  
461  
462 Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val  
463 385 390 395  
464  
465 Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp  
466 400 405 410  
467  
468 Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser  
469 415 420  
470  
471 Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala  
472 425 430 435  
473  
474 Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys  
475 440 445  
476  
477 Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly

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478 450                      455                      460
479
480 Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
481      465                      470                      475
482
483 Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
484      480                      485
485
486 Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
487      490                      495                      500
488
489 Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
490      505                      510
491
492 Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
493 515                      520                      525
494
495 Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
496      530                      535                      540
497
498 Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
499      545                      550
500
501 Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
502      555                      560                      565
503
504 Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
505      570                      575
506
507 Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
508 580                      585                      590
509
510 Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
511      595                      600                      605
512
513 His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
514      610                      615
515
516 Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
517      620                      625                      630
518
519 Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
520      635                      640
521
522 His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
523 645                      650                      655
524
525 Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
526      660                      665                      670
527
528 Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
529      675                      680
530

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531 Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro  
532 685 690 695  
533  
534 Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu  
535 700 705  
536  
537 Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys  
538 710 715 720  
539  
540 Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val  
541 725 730 735  
542  
543 Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys  
544 740 745  
545  
546 Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly  
547 750 755 760  
548  
549 Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp  
550 765 770  
551  
552 Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe  
553 775 780 785  
554  
555  
556 Ile Lys Asp Gln Ser Ala Leu End  
557 790

Invalid

Pls. delete

PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/621,092B

DATE: 05/02/91  
TIME: 11:24:18

LINE ERROR

ORIGINAL TEXT

556 Wrong Amino Acid Designator

Ile Lys Asp Gln Ser Ala Leu End

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/621,092B

DATE: 05/02/91  
TIME: 11:24:18

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/621,092B

DATE: 05/02/91  
TIME: 11:24:18

LINE ORIGINAL TEXT

CORRECTED TEXT

59 (2) INFORMATION FOR SEQ ID NO:1  
87 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:1  
341 (3) INFORMATION FOR SEQ ID NO:2  
367 (vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

(2) INFORMATION FOR SEQ ID NO:1:  
(vi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
(3) INFORMATION FOR SEQ ID NO:2:  
(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2: